REMARKS

Applicants respectfully request entry of this amendment. An Associate Power of Attorney is submitted herewith. Preliminarily, the specification is amended herein to correct an obvious error in which two residues in SEQ ID NO:10 were inadvertently juxtaposed. The accurate amino acid sequence is fully supported by Figures 3 and 4 of the application as filed. A Substitute Sequence Listing reflecting the amendment to the specification accompanied by a Statement to Support Filing and Submission in Accordance with 37 C.F.R. §§ 1.821 through 1.825 is submitted herewith. Entry thereof is respectfully requested. The amendment to the specification also corrects an obvious error made in the previous preliminary amendment in which text was inadvertently omitted during transcribing. The amendment is supported by the specification as filed at page 53, lines 31-38. Accordingly Applicants submit that the amendments to the specification do not introduce new matter and are fully supported by the specification as originally filed.

Claims 38-44 are pending in the present application and are subject to a Restriction Requirement. Applicants respectfully traverse the Restriction Requirement. Applicants submit that examination of the claims of both Groups I and II would not impose a serious burden on the Examiner. Accordingly, Applicants request reconsideration and withdrawal of the restriction requirement. Nonetheless, to be fully responsive, Applicants hereby elect Group I and reserve the right to prosecute the claims of non-elected Group II in future continuing and/or divisional applications.

CONCLUSION

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

Applicants submit that the present claims meet all the requirements for patentability. The Examiner is respectfully requested to allow all the solicited claims. Applicants invite the Examiner to contact the undersigned at (215) 557-5908 to clarify any unresolved issues raised by this response.

Respectfully submitted,

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Date: August 6, 2002

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Attachments:

Paper copy of Sequence Listing (pages 1-18)
Sequence Listing in Computer Readable Form
Statement in Support of Sequence Listing
Version With Markings To Show Changes Made
Associate Power of Attorney

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE TITLE:

Please amend the title to read as follows:

-- HELICOBACTER PYLORI CYTOTOXIN PROTEINS USEFUL FOR VACCINES AND DIAGNOSTICS--.

IN THE SEQUENCE LISTING:

Please insert pages 1-18 of the sequence listing.

IN THE SPECIFICATION:

Please amend the specification as follows:

Please replace the paragraph spanning from page 52, line 15 to page 53, line 9 with the following replacement paragraph.

--The *cai* gene coded for a putative protein of 1147 amino acids, with predicted molecular weight of 128012.73 Daltons and an isoelectric point of 9.72. The basic properties of the purified protein were confirmed by two dimensional gel electrophoresis. The codon usage and the GC content (37%) of the gene were similar to that described for other *H. pylori* genes (13, 26). A putative ribosome binding site: AGGAG, was identified 5 base pairs upstream from the proposed ATG starting codon. Computer search for promoter sequences of the region upstream from the ATG start codon, identified sequences resembling either -10 or -35 regions, however, a region with good consensus to an *E. coli* promoter, or resembling published *H. pylori* promoter sequences was not found. Primer extension analysis of purified *H. pylori* RNA showed that 104 and 214 base pairs upstream from the ATG start codon there are two transcriptional starts sites. Canonical promoters could not be identified upstream from either transcriptional initiation sites. The expression of a portion of the CAI antigen by clone 57/D suggests that *E. coli* is also recognizing a promoter in this region, however, it is not clear whether *E. coli* recognizes the same promoters of *H. pylori* or whether the *H. pylori* DNA that is rich in A-T provides *E. coli* with regions that may act as promoters. A rho independent terminator was identified downstream from the stop codon. In Fig. 4, the AGGAG ribosome binding site and terminator are underlined, and the repeated sequence and motif containing 6 asparagines are boxed. The CAI antigen was very hydrophilic, and did not show obvious leader peptide or transmembrane sequences. The most hydrophilic region was from amino acids 600 to 900, where also a number of unusual features can be observed: the repetition of the sequences EFKNGKNKDFSK (SEQ ID NO:9) and EPIYA [EPYIA]

(SEQ ID NO:10), and the presence of a stretch of six contiguous asparagines (boxed in Fig. 4).--